```
            RAW SEQUENCE LISTING              DATE: 11/06/2001
            PATENT APPLICATION:  US/09/750,240    TIME: 11:09:45

                 Input Set : A:\220002056723.txt
                 Output Set: N:\CRF3\11062001\I750240.raw

      4 <110> APPLICANT: Hammon, H. K.
      5        Insel, P. A.
      6        Ping, P.
      7        Post, S. R.
      8        Gao, M.
     10 <120> TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
     11        FAILURE
     13 <130> FILE REFERENCE: 220002056723
     15 <140> CURRENT APPLICATION NUMBER: US 09/750,240
C--> 16 <141> CURRENT FILING DATE: 2001-10-12
     18 <150> PRIOR APPLICATION NUMBER: US 09/472,667
     19 <151> PRIOR FILING DATE: 1999-12-27
     21 <150> PRIOR APPLICATION NUMBER: US 09/008,097
     22 <151> PRIOR FILING DATE: 1998-01-16
     24 <150> PRIOR APPLICATION NUMBER: US 08/924,757
     25 <151> PRIOR FILING DATE: 1997-09-05
     27 <150> PRIOR APPLICATION NUMBER: US 60/048,933
     28 <151> PRIOR FILING DATE: 1997-06-16
     30 <150> PRIOR APPLICATION NUMBER: US 08/708,661
     31 <151> PRIOR FILING DATE: 1996-09-05
     33 <160> NUMBER OF SEQ ID NOS: 13
     35 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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     43 <221> NAME/KEY: misc_feature
     44 <222> LOCATION: (1)...(314)
     45 <223> OTHER INFORMATION: n = A,T,C or G
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     50 ccccgctata tgagctgcct ccgggatgca gagccaccca gccccacccc tgcgggcccc   180
W--> 51 cctcggtgcc cctggcagga tgacgccttc atccggaggg gcggcccang caagggcaag   240
     52 gaactggggc tgcgggcagt ggccctgggc ttcgaagata ccgaagtgac aacgacaccg   300
     53 gcgggaccgc tgaa                                                     314
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     56 <211> LENGTH: 104
     57 <212> TYPE: PRT
     58 <213> ORGANISM: Homo sapiens
     60 <220> FEATURE:
     61 <221> NAME/KEY: VARIANT
     62 <222> LOCATION: (1)...(104)
     63 <223> OTHER INFORMATION: Xaa = Any Amino Acid
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RAW SEQUENCE LISTING   DATE: 11/06/2001
PATENT APPLICATION: US/09/750,240   TIME: 11:09:45

Input Set : A:\220002056723.txt
Output Set: N:\CRF3\11062001\I750240.raw

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68 Thr Ala Trp Gly Glu Arg Asn Gly Gln Lys Arg Ser Arg Arg Arg Gly
69             20                 25                 30
70 Thr Arg Ala Gly Gly Phe Cys Thr Pro Arg Tyr Met Ser Cys Leu Arg
71         35                 40                 45
72 Asp Ala Glu Pro Pro Ser Pro Thr Pro Ala Gly Pro Pro Arg Cys Pro
73      50                 55                 60
74 Trp Gln Asp Asp Ala Phe Ile Arg Arg Gly Gly Pro Xaa Lys Gly Lys
75 65                 70                 75                 80
76 Glu Leu Gly Leu Arg Ala Val Ala Leu Gly Phe Glu Asp Thr Glu Val
77             85                 90                 95
78 Thr Thr Thr Pro Ala Gly Pro Leu
79             100
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W--> (line 74)   Oر

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82 <211> LENGTH: 1812
83 <212> TYPE: DNA
84 <213> ORGANISM: Homo sapiens
86 <400> SEQUENCE: 3
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88  ccgcgcagcc cctctgcggg cctctggtgc cctgtgttct ttgtatacat cgcatacacg     120
89  ctcctcccca tccgcatgcg ggctgccgtc ctcagcggcc tgggcctctc caccttgcat     180
90  ttgatcttgg cctggcaact taaccgtggt gatgccttcc tctggaagca gctcggtgcc     240
91  aatgtgctgc tgttcctctg caccaacgtc attagcatct gcacacacta tccagcagag     300
92  gtgtctcagc gccaggcctt tcaggagacc cgcagttaca tccaggcccg gctccacctg     360
93  cagcatgaga atcggcagca ggagcggctg ctgctgtcgg tattgcccca gcacgttgcc     420
94  atggagatga agaagacat caacacaaaa aaagaagaca tgttccacaa gatctacata     480
95  cagaagcatg acaatgtcag catcctgttt gcagacattg agggcttcac cagcctggca     540
96  tcccagtgca ctgcgcagga gctggtcatg accctgaatg agctctttgc ccggtttgac     600
97  aagctggctg cggagaatca ctgcctgagg atcaagatct tgggggactg ttactactgt     660
98  gtgtcagggc tgccggaggc ccgggccgac catgcccact gctgtgtgga gatggggta     720
99  gacatgattg aggccatctc gctggtacgt gaggtgacag gtgtgaatgt gaacatgcgc     780
100 gtgggcatcc acagcgggcg cgtgcactgc ggcgtccttg gcttgcggaa atggcagttc     840
101 gatgtgtggt ccaatgatgt gaccctggcc aaccacatgg aagcaggaag ccgggctggc     900
102 cgcatccaca tcactcgggc aacactgcag tacctgaacg gggactacga agtggagcca     960
103 ggccgtggtg gcaagcgcaa cgcgtacctc aaggagcagc acattgagac tttcctcatc    1020
104 ctgggcgcca gccagaaacg gaaagaggag aaaggcatgc tggccaagct gcagcggact    1080
105 cgggccaact ccatggaagg gctgatgccg cgatgggttc ctgatcgtgc cttctcccgg    1140
106 accaaggact ccaaggcctt ccgccagatg ggcattgatg attccagcaa agacaaccgg    1200
107 ggcacccaag atgccctgaa ccctgaggat gaggtggatg agttcctgag ccgtgccatc    1260
108 gatgcccgca gcattgatca gctgcggaag gaccatgtgc gccggttttt gctcaccttc    1320
109 cagagagagg attttgagaa gaagtactcc cggaaggtgg atccccgctt cggagcctac    1380
110 gttgcctgtg ccctgttggt cttctgcttc atctgcttca tccagcttct aattttccca    1440
111 cactccaccc tgatgcttgg gatttatgcc agcatcttcc tgctgctgct aatcaccgtg    1500
112 ctgatctgtg ctgtgtactc ctgtggttct ctgttcccta aggccctgca acgtctgtcc    1560
113 cgcagcattg tccgctcacg ggcacatagc accgcagttg gcatcttttc cgtcctgctt    1620
114 gtgtttactt ctgccattgc caacatgttc acctgtaacc acacccccat acggagctgt    1680
115 gcagcccgga tgctgaattt aacacctgct gacatcactg cctgccacct gcagcagctc    1740
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```

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128             20                  25                  30
129 Phe Phe Val Tyr Ile Ala Tyr Thr Leu Leu Pro Ile Arg Met Arg Ala
130         35                  40                  45
131 Ala Val Leu Ser Gly Leu Gly Leu Ser Thr Leu His Leu Ile Leu Ala
132     50                  55                  60
133 Trp Gln Leu Asn Arg Gly Asp Ala Phe Leu Trp Lys Gln Leu Gly Ala
134 65                  70                  75                  80
135 Asn Val Leu Leu Phe Leu Cys Thr Asn Val Ile Ser Ile Cys Thr His
136             85                  90                  95
137 Tyr Pro Ala Glu Val Ser Gln Arg Gln Ala Phe Gln Glu Thr Arg Ser
138             100                 105                 110
139 Tyr Ile Gln Ala Arg Leu His Leu Gln His Glu Asn Arg Gln Gln Glu
140         115                 120                 125
141 Arg Leu Leu Leu Ser Val Leu Pro Gln His Val Ala Met Glu Met Lys
142     130                 135                 140
143 Glu Asp Ile Asn Thr Lys Lys Glu Asp Met Phe His Lys Ile Tyr Ile
144 145                 150                 155                 160
145 Gln Lys His Asp Asn Val Ser Ile Leu Phe Ala Asp Ile Glu Gly Phe
146             165                 170                 175
147 Thr Ser Leu Ala Ser Gln Cys Thr Ala Gln Glu Leu Val Met Thr Leu
148             180                 185                 190
149 Asn Glu Leu Phe Ala Arg Phe Asp Lys Leu Ala Ala Glu Asn His Cys
150         195                 200                 205
151 Leu Arg Ile Lys Ile Leu Gly Asp Cys Tyr Tyr Cys Val Ser Gly Leu
152     210                 215                 220
153 Pro Glu Ala Arg Ala Asp His Ala His Cys Cys Val Glu Met Gly Val
154 225                 230                 235                 240
155 Asp Met Ile Glu Ala Ile Ser Leu Val Arg Glu Val Thr Gly Val Asn
156             245                 250                 255
157 Val Asn Met Arg Val Gly Ile His Ser Gly Arg Val His Cys Gly Val
158             260                 265                 270
159 Leu Gly Leu Arg Lys Trp Gln Phe Asp Val Trp Ser Asn Asp Val Thr
160         275                 280                 285
161 Leu Ala Asn His Met Glu Ala Gly Ser Arg Ala Gly Arg Ile His Ile
162     290                 295                 300
163 Thr Arg Ala Thr Leu Gln Tyr Leu Asn Gly Asp Tyr Glu Val Glu Pro
164 305                 310                 315                 320
165 Gly Arg Gly Gly Lys Arg Asn Ala Tyr Leu Lys Glu Gln His Ile Glu
166             325                 330                 335
167 Thr Phe Leu Ile Leu Gly Ala Ser Gln Lys Arg Lys Glu Glu Lys Gly
168         340                 345                 350
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RAW SEQUENCE LISTING   DATE: 11/06/2001
PATENT APPLICATION: US/09/750,240   TIME: 11:09:45

Input Set : A:\220002056723.txt
Output Set: N:\CRF3\11062001\I750240.raw

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170         355             360             365
171 Met Pro Arg Trp Val Pro Asp Arg Ala Phe Ser Arg Thr Lys Asp Ser
172     370             375             380
173 Lys Ala Phe Arg Gln Met Gly Ile Asp Asp Ser Ser Lys Asp Asn Arg
174 385             390             395             400
175 Gly Thr Gln Asp Ala Leu Asn Pro Glu Asp Glu Val Asp Glu Phe Leu
176             405             410             415
177 Ser Arg Ala Ile Asp Ala Arg Ser Ile Asp Gln Leu Arg Lys Asp His
178             420             425             430
179 Val Arg Arg Phe Leu Leu Thr Phe Gln Arg Glu Asp Phe Glu Lys Lys
180         435             440             445
181 Tyr Ser Arg Lys Val Asp Pro Arg Phe Gly Ala Tyr Val Ala Cys Ala
182     450             455             460
183 Leu Leu Val Phe Cys Phe Ile Cys Phe Ile Gln Leu Leu Ile Phe Pro
184 465             470             475             480
185 His Ser Thr Leu Met Leu Gly Ile Tyr Ala Ser Ile Phe Leu Leu Leu
186             485             490             495
187 Leu Ile Thr Val Leu Ile Cys Ala Val Tyr Ser Cys Gly Ser Leu Phe
188             500             505             510
189 Pro Lys Ala Leu Gln Arg Leu Ser Arg Ser Ile Val Arg Ser Arg Ala
190         515             520             525
191 His Ser Thr Ala Val Gly Ile Phe Ser Val Leu Leu Val Phe Thr Ser
192     530             535             540
193 Ala Ile Ala Asn Met Phe Thr Cys Asn His Thr Pro Ile Arg Ser Cys
194 545             550             555             560
195 Ala Ala Arg Met Leu Asn Leu Thr Pro Ala Asp Ile Thr Ala Cys His
196             565             570             575
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204 <212> TYPE: DNA
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210 cccgctata tgagctgcct ccgggatgca gagccaccca gccccacccc tgcgggcccc       180
211 cctcggtgcc cctggcagga tgacgccttc atccggaggg gcggcccagg caagggcaag       240
212 gagctggggc tgcgggcagt ggccctgggc ttcgaggata ccgaggtgac aacgacagcg       300
213 ggcgggacgg ctgaggtggc gcccgacgcg gtgcccagga gtgggcgatc ctgctggcgc       360
214 cgtttggtgc aggtgttcca gtcgaagcag ttccgttcgg ccaagctgga gcgcctgtac       420
215 cagcggtact tttttccagat gaaccagagc agcctgacgc tgctggtggc ggtgctggtg       480
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217 gtggcactgt tggcctgtgc cgccgccctg ttcgtggggc tcatggtggt gtgtaaccgg       600
218 catagcttcc gccaggactc catgtgggtg gtgagtaacg tggtgctggg catcctggcg       660
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220 tgccctgtgt tctttgtata catcgcatac acgctcctcc ccatccgcat gcgggctgcc   780
221 gtcctcagcg gcctgggcct ctccaccttg catttgatct tggcctggca acttaaccgt   840
222 ggtgatgcct tcctctggaa gcagctcggt gccaatgtgc tgctgttcct ctgcaccaac   900
223 gtcattagca tctgcacaca ctatccagca gaggtgtctc agcgccaggc ctttcaggag   960
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243 gccagcatct tcctgctgct gctaatcacc gtgctgatct gtgctgtgta ctcctgtggt  2160
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252 gatggctgg actgtccagc tgcagggagg gtggccctca aatatatgac ccctgtgatt  2700
253 ctgctggtgt ttgcgctggc gctgtatctg catgctcagc aggtggaatc gactgcccgc  2760
254 ctaaacttcc tctggaaact acaggcaaca ggggaaaaag aggagatgga ggagctacag  2820
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269 <210> SEQ ID NO: 6
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VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/750,240**

DATE: 11/06/2001
TIME: 11:09:46

Input Set : **A:\220002056723.txt**
Output Set: **N:\CRF3\11062001\I750240.raw**

L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:51 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:74 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2